(L) selecting for interaction by transferring host cells or progeny of host cells in step (E) to

(v) at least one selective medium, wherein said selective medium that precludes growth of host cells in the presence of the first counterselectable marker of the counterselectable markers specified in (K) and allows growth in the presence of a first selectable marker;

(vi) at least one selective medium, wherein said selective medium precludes growth of host cells in the presence of the second counterselectable marker of the counterselectable markers specified in (K) and allows growth in the presence of a second selectable marker;

(vii) a further selective medium that allows identification of said host cells upon activation of the readout system; and

(M) identifying host cells that contain molecules that:

(viii) do not activate said readout system on said at least one selective medium specified in (v); and

(ix) do not activate said readout system on said at least one selective medium specified in (vi); and

(x) activate said readout system on said selective medium specified in (vii).

50 [3]. The method of claim 49, wherein said at least two genetic elements that additionally comprise a counterselectable marker further specify a DNA binding domain fusion protein and an activation domain fusion protein, respectively.

51 [4]. The method of claim 47, wherein said counterselectable marker or counterselectable markers of step (H) or (K) are selected from the group of URA3, LYS2, sacB, CAN1, CYH2, rpsL or lacY.

52 [5]. The method of claim 47, wherein the transfer of host cells or progeny of host cells in step (I) or (L) is effected or assisted by automation.

53 [6]. The method of claim 52, wherein the said automation in step (I) or (L) is effected by an automated replicating, picking, spotting, pipetting or micropipetting or cell sorting device.